

## SEQUENCE LISTING

<110> Rittershaus, Charles W.  
Thomas, Lawrence J.  
Avant Immunotherapeutics, Inc.

<120> Xenogeneic Cholesteryl Ester Transfer Protein (CETP)  
for Modulation of CETP Activity

<130> TCS-420.1 PCT seqlist

<140> PCT/US98/22145

<141> 1998-10-20

<150> 08/954,643

<151> 1997-10-20

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 476

<212> PRT

<213> Homo sapiens

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<301> Drayna, Dennis

<302> Cloning and Sequencing of Human Cholesteryl Ester  
Transfer cDNA

<303> Nature

<304> 327

<306> 632-634

<307> 1987-06-18

<313> 1 TO 476

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Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala Lys Val Ile Gln  
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Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr Gly Glu Lys Ala  
35 40 45

Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile  
50 55 60

Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu Ala Lys  
 65 70 75 80

Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr  
 85 90 95

Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Trp Leu Gly Ile Asp Gln Ser  
 100 105 110

Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln  
 115 120 125

Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys Tyr  
 130 135 140

Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro  
 145 150 155 160

Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys  
 165 170 175

Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Val Ile Ser Asn  
 180 185 190

Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp  
 195 200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr  
 210 215 220

Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe Ile Tyr Lys Asn  
 225 230 235 240

Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu Leu Gly  
 245 250 255

Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser  
 260 265 270

Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser Leu Met  
 275 280 285

Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr Asn  
 290 295 300

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln  
 305 310 315 320

Val Thr Val His Cys Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys  
 325 330 335  
 Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro Arg  
 340 345 350  
 Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile Val  
 355 360 365  
 Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu  
 370 375 380  
 Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu Ser  
 385 390 395 400  
 Ser Ser Glu Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val  
 405 410 415  
 Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe Thr Ala Leu  
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 Met Asn Ser Lys Gly Val Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile  
 435 440 445  
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 Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
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&lt;210&gt; 2

&lt;211&gt; 1428

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;300&gt;

&lt;301&gt; Drayna, Dennis

 <302> Cloning and Sequencing of Human Cholesteryl Ester  
 Transfer cDNA

&lt;303&gt; Nature

&lt;304&gt; 327

&lt;306&gt; 632-634

&lt;307&gt; 1987-06-18

&lt;313&gt; 1 TO 476

&lt;400&gt; 2

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 ccagatatca cgggcgagaa ggccatgatg ctccctggcc aagtcaagta tgggttgac 180  
 aacatccaga tcagccactt gtccatcgcc agcagccagg tggagctggt ggaagccaag 240  
 tccattgatg tctccattca gaacgtgtct gtggtcttca aggggaccct gaagtatggc 300  
 tacaccactg cctggtggct ggggtattgat cagtccattg acttcgagat cgactctgcc 360  
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&lt;210&gt; 3

&lt;211&gt; 496

&lt;212&gt; PRT

<213> *Oryctolagus cuniculus*

&lt;300&gt;

&lt;301&gt; Nagashima, Mariko

 <302> Cloning and mRNA tissue distribution of rabbit  
 cholesteryl ester transfer protein

&lt;303&gt; J. Lipid Res.

&lt;304&gt; 29

&lt;306&gt; 1643-1649

&lt;307&gt; 1988

&lt;313&gt; 1 TO 496

&lt;400&gt; 3

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Lys	Pro	Ala	Leu	Leu	Val	Leu	Asn	Gln	Glu	Thr	Ala	Lys	Val	Val	Gln
			20					25					30		

Thr	Ala	Phe	Gln	Arg	Ala	Gly	Tyr	Pro	Asp	Val	Ser	Gly	Glu	Arg	Ala
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35 40 45

Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile  
50 55 60

Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala Lys  
65 70 75 80

Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr  
85 90 95

Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln Ser  
100 105 110

Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu  
115 120 125

Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys Tyr  
130 135 140

Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro  
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Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys  
165 170 175

Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser Asn  
180 185 190

Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp  
195 200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr  
210 215 220

Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys Asn  
225 230 235 240

Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu Gly  
245 250 255

Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser  
260 265 270

Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu Thr  
275 280 285

Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr Asn

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 Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala  
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 Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn  
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 Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe Pro  
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 Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile  
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 Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His  
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 Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser Ser  
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                     450                      455                      460  
 Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp  
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&lt;211&gt; 1488

&lt;212&gt; DNA

<213> *Oryctolagus cuniculus*

&lt;300&gt;

<301> Nagashima, Mariko  
 <302> Cloning and mRNA tissue distribution of rabbit  
 cholesteryl ester transfer protein  
 <303> J. Lipid Res.  
 <304> 29  
 <306> 1643-1649  
 <307> 1988  
 <313> 1 TO 496

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 ccggacgtca gcggcgagag ggccgtgatg ctccctggcc ggggtcaagta cgggctgcac 180  
 aacctccaga tcagccacct gtccatcgcc agcagccagg tggagctggt ggacgccaaag 240  
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 cccgactgct acctggcttt ccataaactg ctccctgcacc tccaggggga gcgcgagccg 480  
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 gtctccgagg ccttccccct cgcgccttc cgcgccgtc ttctggggga ctcccgcatg 780  
 ctctacttct ggttctccga tcaagtgtc aactccctgg ccaggggcgc cttccaggag 840  
 ggccgtctcg tgctcagcct gacaggggat gaggttcaaga aagtgtctga gaccaggggt 900  
 ttcgacacca accaggaaat cttccaggag ctttccagag gccttccac cggccaggcc 960  
 caggtagccg tccactgcct taagtgccc aagatctct gccagaaccg ggggtgtctg 1020  
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 ttcgaaatca tcaaccccca gattatcact ctcatgggt gcctgctgct gcagatggac 1440  
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: humanized  
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Lys Pro Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Val Gln  
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 Thr Ala Phe Gln Arg Ala Gly Tyr Pro Asp Val Ser Gly Glu Arg Ala  
 35 40 45  
 Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile  
 50 55 60  
 Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala Lys  
 65 70 75 80  
 Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr  
 85 90 95  
 Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln Ser  
 100 105 110  
 Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu  
 115 120 125  
 Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys Tyr  
 130 135 140  
 Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro  
 145 150 155 160  
 Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys  
 165 170 175  
 Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser Asn  
 180 185 190  
 Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp  
 195 200 205  
 Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr  
 210 215 220  
 Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys Asn  
 225 230 235 240  
 Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu Gly  
 245 250 255  
 Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser  
 260 265 270



Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu Thr  
275 280 285

Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr Asn  
290 295 300

Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala  
305 310 315 320

Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn  
325 330 335

Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe Pro  
340 345 350

Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile  
355 360 365

Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His  
370 375 380

Leu Leu Asp Phe Gln Cys Val Pro Lys Ala Val Ser Asn Leu Thr Glu  
385 390 395 400

Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser Leu Ile Ala Thr  
405 410 415

Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Ala Phe Thr Ala  
420 425 430

Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu  
435 440 445

Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe Gly Phe  
450 455 460

Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
465 470 475

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<211> 496

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: humanized

## rabbit CESTP protein

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 20 25 30  
 Thr Ala Phe Gln Arg Ala Gly Tyr Pro Asp Val Ser Gly Glu Arg Ala  
 35 40 45  
 Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile  
 50 55 60  
 Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala Lys  
 65 70 75 80  
 Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr  
 85 90 95  
 Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln Ser  
 100 105 110  
 Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu  
 115 120 125  
 Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys Tyr  
 130 135 140  
 Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro  
 145 150 155 160  
 Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys  
 165 170 175  
 Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser Asn  
 180 185 190  
 Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp  
 195 200 205  
 Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr  
 210 215 220  
 Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys Asn  
 225 230 235 240

Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu Gly  
 245 250 255  
 Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser  
 260 265 270  
 Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu Thr  
 275 280 285  
 Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr Asn  
 290 295 300  
 Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala  
 305 310 315 320  
 Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn  
 325 330 335  
 Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe Pro  
 340 345 350  
 Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile  
 355 360 365  
 Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His  
 370 375 380  
 Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser Ser  
 385 390 395 400  
 Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn  
 405 410 415  
 Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser Leu  
 420 425 430  
 Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Ala  
 435 440 445  
 Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile Ile  
 450 455 460  
 Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp  
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 Phe Gly Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
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<210> 7

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: fusion protein  
of a tetanus toxoid segment and human CTFP  
C-terminus

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1 5 10 15

Gly Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
20 25 30